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amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

57. A method of claim 56, wherein the database comprises quantitative gene expression information from liver cell or tissue samples that have been exposed to amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-1464.

58. A method of claim 55, wherein the database comprises quantitative gene expression information for at least one gene that's expression is correlated in the database with a hepatitis liver pathology.

59. A method of claim 55, wherein the database comprises quantitative gene expression information for at least one gene that's expression is correlated in the database with liver necrosis without fatty liver pathology.

60. A method of claim 55, wherein the database comprises quantitative gene expression information for at least one gene that's expression is correlated in the database with liver necrosis with fatty liver pathology.

61. A method of claim 55, wherein the database comprises quantitative gene expression information for at least one gene that's expression is correlated in the database with a liver pathology induced by a toxin that is a protein adduct former.

62. A method of claim 55, wherein step (b) comprises comparing the expression level for at least one gene in the expression profile to the mean expression level for that gene in the database.

63. A method of claim 55, wherein step (b) further comprises comparing the expression level for at least one gene in the expression profile to the mean expression level for that gene in control samples.

64. A method of claim 55, wherein the gene expression profile comprises the expression level for at least one gene from a cell or tissue sample exposed to the compound.

65. A method of claim 55, wherein the gene expression profile comprises the expression level for at least about ten genes from a cell or tissue sample exposed to the compound.

66. A method of claim 55, wherein the gene expression profile comprises the expression level for at least about 50 genes from a cell or tissue sample exposed to the compound.

67. A method of claim 55, wherein the gene expression profile comprises the expression level for at least about 100 genes from a cell or tissue sample exposed to the compound.

68. A method of claim 55, wherein the gene expression profile is produced by hybridization of nucleic acids from a cell or tissue sample exposed to the compound to a nucleic acid microarray.

69. A method of claim 55, wherein the quantitative gene expression in the database is produced from hybridization of nucleic acids from a liver cell or tissue sample that has been exposed to at least one toxin to a nucleic acid microarray.

70. A method of claim 55, wherein the gene expression profile is produced by quantitative or semi-quantitative amplification of nucleic acids from a cell or tissue sample exposed to the compound.

71. A method of claim 55, wherein the toxic effect is selected from the group consisting of liver damage induced by hepatitis, liver damage induced by NSAIDS, liver necrosis with fatty liver, liver necrosis without fatty liver and liver damage induced by protein adduct

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formers.

72. A method of claim 55, wherein the toxic effect is substantially similar to that induced by a toxin selected from the group consisting of amitriptyline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-1464.

73. A method of claim 55, wherein the database comprises quantitative gene expression information for at least about 10 genes.

74. A method of claim 55, wherein the database comprises quantitative gene expression information for at least about 100 genes.

75. A method of claim 55, wherein the database further comprises sequence information for the genes in the database.

76. A method of claim 55, wherein the database further comprises descriptive information from an external database which correlates the genes in the database to the records in the external database.

77. A method of claim 55, wherein the database comprises mean expression values from liver cell or tissue samples that have been exposed to at least one toxin and mean expression values from control liver cell or tissue samples that have not been exposed to a toxin.

78. A method of claim 77, wherein the database comprises at least part of the information in Tables 3A-3S.

79. A method of claim 77, wherein the database comprises substantially all of the information in Tables 3A-3S.

80. A method of claim 77, wherein the database comprises all of the information in

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Tables 3A-3S.

81. A method of claim 77, wherein the database further comprises information that measures the ability of each gene to predict whether or not a sample has been exposed to a toxin.

82. A method of claim 81, wherein the information comprises a linear discriminant analysis score for each gene.

83. A method of claim 77, wherein the mean values are derived from average difference values calculated for each gene averaged across the liver cell or tissue samples that have not been exposed to a toxin or a control.

84. A method of claim 55, wherein the toxic effect comprises modulation of a metabolic pathway of Table 1.

85. A method of claim 55, wherein the toxicity is hepatotoxicity.

86. A method of predicting the hepatotoxicity of a compound, comprising:

(a) preparing a gene expression profile from a liver cell or tissue sample exposed to the compound; and

(b) comparing the gene expression profile to a database comprising quantitative gene expression information from a liver cell or tissue sample that has been exposed to at least one hepatotoxin.

87. A method of claim 86, wherein the toxin is selected from the group consisting of amitriptyline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

88. A method of predicting the hepatotoxicity of a compound, comprising:

(a) preparing a gene expression profile from a liver cell or tissue sample exposed to the compound; and